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TECH CENTER 1600/291



SEQUENCE LISTING

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<120> Means and Methods for Fibroblast-Like or Macrophage-Like Cell  
Transduction

<130> 2183-3982.2US

<140> 09/517,898

<141> 2000-03-03

<150> 60/122,732

<151> 1999-03-03

<160> 35

<170> PatentIn version 3.1

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27

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25

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27

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<210> 20  
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<210> 31	
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<212> DNA	
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<211> 1068	
<212> DNA	
<213> Adenovirus Ad5/fib16 Chimeric Fiber	
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agcagctcac aacacccctt tataaaccct ggttcattt cctcaaatgg tttgcacaa	120
agcccagatg gagttctaac tcttaaatgt gttaatccac tcactaccgc cagcggaccc	180
ctccaactta aagttggaag cagtcattaca gtagatacta tcgatggtc tttggaggaa	240
aatataactg ccgaagcgcc actcactaaa ctaaccactc catagttta ttaataggat	300
ctggcttgca aacaaaggat gataaacttt gtttatcgct gggagatggg ttggtaacaa	360
aggatgataa actatgtta tcgctggag atgggttaat aacaaaaaat gatgtactat	420
gtgccaaact aggacatggc cttgtgtttg actcttccaa tgctatcacc atagaaaaca	480
acaccttgc gacaggcgca aaaccaagcg ccaactgtgt aattaaagag ggagaagatt	540
ccccagactg taagctact ttagttctag tgaagaatgg aggactgata aatggataca	600
taacattaat gggagcctca gaatatacta acaccttgc taaaacaatc aagttacaat	660
cgtatgaaac ctcgcatttgc ataatactgg ccaaattatt acttacctat catcccttaa	720
aagtaacctg aactttaaag acaacaaaa catggctact ggaaccataa ccagtgc当地	780
aggcttcatg cccagcacca ccgcctatcc atttataaca tacgccactg agaccctaa	840
tgaagattac atttatggag agtgttacta caaatctacc aatggaaactc tctttccact	900
aaaagttact gtcacactaa acagacgtat gtttagcttgc ggaatggct atgctatgat	960
ttttcatggc ctctaaatgc agaggaagcc ccggaaaacta ccgaagtcac ttcattacc	1020
tcccccatttctt ttttttctta tatcagagaa gatgactgaa tgcattag	1068

<210> 33  
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<213> Adenovirus Ad16 Fiber

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agcagctcac aacaccctt tataaaccctt gtttcattt cctcaaatttgg ttttgcacaa 120  
agccccagatg gagttctaac ttctaaatgtt gttaatccac tcactaccgc cagcggaccc 180  
ctccaaactt aagtggaaag cagtcttaca gtagatacta tcgatgggtc tttggaggaa 240  
aatataactg ccgcagcgcc actcactaaa actaaccact ccataggttt attaatagga 300  
tctggcttgc aaacaaagga tgataaaactt tgtttatcgc tggagatgg gttggttaaca 360  
aaggatgata aactatgttt atcgctggga gatgggttaa taacaaaaaa tgatgtacta 420  
tgtgccaaac taggacatgg ccttgtgttt gactcttcca atgctatcac catagaaaac 480  
aacaccccttggacaggcgcaaaaaccaagc gccaactgtg taattaaaga gggagaagat 540  
tccccagact gtaagctcac tttagttcta gtgaagaatg gaggactgat aaatggatac 600  
ataacattaa tggagcctc agaatataact aacaccccttggtaaaca tcaagttaca 660  
atcgatgtaa acctcgcat tgataatactt gccaatttttacatccctt 720  
aaaagtaacc tgaactttaa agacaaccaa aacatggcta ctggaaaccat aaccagtgcc 780  
aaaggcttca tgcccagcac caccgcctat ccattataa catacgccac tgagacccta 840  
aatgaagatt acatttatgg agagtgttac tacaatcta ccaatggaaac tctcttcca 900  
ctaaaaagtttca ctgtcacact aaacagacgt atgttagctt ctggaaatggc ctatgctatg 960  
aatttttcat ggtctctaaa tgcagaggaa gccccggaaa ctaccgaagt cactctcat 1020  
acccccccttcttttttc ttatatcaga gaagatgact ga 1062

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<211> 353  
<212> PRT  
<213> Chimaeric Ad5/Fib16

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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
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Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe  
20 25 30

Ile Ser Ser Asn Gly Phe Ala Gln Ser Pro Asp Gly Val Leu Thr Leu  
35 40 45

Lys Cys Val Asn Pro Leu Thr Thr Ala Ser Gly Pro Leu Gln Leu Lys  
50 55 60

Val Gly Ser Ser Leu Thr Val Asp Thr Ile Asp Gly Ser Leu Glu Glu  
65 70 75 80

Asn Ile Thr Ala Ala Ala Pro Leu Thr Lys Thr Asn His Ser Ile Gly  
85 90 95

Leu Leu Ile Gly Ser Gly Leu Gln Thr Lys Asp Asp Lys Leu Cys Leu  
100 105 110

Ser Leu Glu Asp Gly Leu Val Thr Lys Asp Asp Lys Leu Cys Leu Ser  
115 120 125

Leu Gly Asp Gly Leu Ile Thr Lys Asn Asp Val Leu Cys Ala Lys Leu  
130 135 140

Gly His Gly Leu Val Phe Asp Ser Ser Asn Ala Ile Thr Ile Glu Asn  
145 150 155 160

Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile Lys  
165 170 175

Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val Lys  
180 185 190

Asn Gly Gly Leu Ile Asn Gly Tyr Ile Thr Leu Met Gly Ala Ser Glu  
195 200 205

Tyr Thr Asn Thr Leu Phe Lys Asn Asn Gln Val Thr Ile Asp Val Asn  
210 215 220

Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser Leu  
225 230 235 240

Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly Thr  
245 250 255

Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Phe  
260 265 270

Ile Thr Tyr Ala Thr Glu Thr Leu Asn Glu Asp Tyr Ile Tyr Gly Glu  
275 280 285

Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val Thr  
290 295 300

Val Thr Leu Asn Arg Arg Met Leu Ala Ser Gly Met Ala Tyr Ala Met  
305 310 315 320

Asn Phe Ser Trp Ser Leu Asn Ala Glu Ala Pro Glu Thr Thr Glu  
325 330 335

Val Thr Leu Ile Thr Ser Pro Phe Phe Ser Tyr Ile Arg Glu Asp  
340 345 350

Asp

<210> 35

<211> 353

<212> PRT

<213> Adenovirus Ad16/Fiber

<400> 35

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Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe  
20 25 30

Ile Ser Ser Asn Gly Phe Ala Gln Ser Pro Asp Gly Val Leu Thr Leu  
35 40 45

Lys Cys Val Asn Pro Leu Thr Thr Ala Ser Gly Pro Leu Gln Leu Lys  
50 55 60

Val Gly Ser Ser Leu Thr Val Asp Thr Ile Asp Gly Ser Leu Glu Glu  
65 70 75 80

Asn Ile Thr Ala Ala Ala Pro Leu Thr Lys Thr Asn His Ser Ile Gly  
85 90 95

Leu Leu Ile Gly Ser Gly Leu Gln Thr Lys Asp Asp Lys Leu Cys Leu  
100 105 110

Ser Leu Glu Asp Gly Leu Val Thr Lys Asp Asp Lys Leu Cys Leu Ser  
115 120 125

Leu Gly Asp Gly Leu Ile Thr Lys Asn Asp Val Leu Cys Ala Lys Leu  
130 135 140

Gly His Gly Leu Val Phe Asp Ser Ser Asn Ala Ile Thr Ile Glu Asn  
145 150 155 160

Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile Lys  
165 170 175

Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val Lys  
180 185 190

Asn Gly Gly Leu Ile Asn Gly Tyr Ile Thr Leu Met Gly Ala Ser Glu  
195 200 205

Tyr Thr Asn Thr Leu Phe Lys Asn Asn Gln Val Thr Ile Asp Val Asn  
210 215 220

Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser Leu  
225 230 235 240

Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly Thr  
245 250 255

Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Phe  
260 265 270

Ile Thr Tyr Ala Thr Glu Thr Leu Asn Glu Asp Tyr Ile Tyr Gly Glu  
275 280 285

Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val Thr  
290 295 300

Val Thr Leu Asn Arg Arg Met Leu Ala Ser Gly Met Ala Tyr Ala Met  
305 310 315 320

Asn Phe Ser Trp Ser Leu Asn Ala Glu Glu Ala Pro Glu Thr Thr Glu  
325 330 335

Val Thr Leu Ile Thr Ser Pro Phe Phe Ser Tyr Ile Arg Glu Asp  
340 345 350

Asp